



SEQUENCE LISTING

<110> Gish, Kurt
Mack, David

<120> Novel Methods of Diagnosing Breast Cancer, Compositions, and Methods
of Screening for Breast Cancer Modulators

<130> A-69028/DJB/JJD

<140> US 09/747,371

<141> 2000-12-21

<150> PCT/ US/00/06952

<151> 2000-03-15

<160> 4

<170> PatentIn version 3.0

<210> 1

<211> 3737

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (81)..(3080)

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      Met Gly Val Ala Gly Arg Asn Arg Pro Gly Ala
      1              5              10

gcc tgg gcg gtg ctg ctg ctg ctg ctg ctg ctg ccg cca ctg ctg ctg      161
Ala Trp Ala Val Leu Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Leu
      15              20              25

ctg gcg ggg gcc gtc ccg ccg ggt cgg ggc cgt gcc gcg ggg ccg cag      209
Leu Ala Gly Ala Val Pro Pro Gly Arg Gly Arg Ala Ala Gly Pro Gln
      30              35              40

gag gat gta gat gag tgt gcc caa ggg cta gat gac tgc cat gcc gac      257
Glu Asp Val Asp Glu Cys Ala Gln Gly Leu Asp Asp Cys His Ala Asp
      45              50              55

gcc ctg tgt cag aac aca ccc acc tcc tac aag tgc tcc tgc aag cct      305
Ala Leu Cys Gln Asn Thr Pro Thr Ser Tyr Lys Cys Ser Cys Lys Pro
      60              65              70              75

ggc tac caa ggg gaa ggc agg cag tgt gag gac atc gat gaa tgt gga      353
Gly Tyr Gln Gly Glu Gly Arg Gln Cys Glu Asp Ile Asp Glu Cys Gly
      80              85              90

aat gag ctc aat gga ggc tgt gtc cat gac tgt ttg aat att cca ggc      401
Asn Glu Leu Asn Gly Gly Cys Val His Asp Cys Leu Asn Ile Pro Gly
      95              100              105

aat tat cgt tgc act tgt ttt gat ggc ttc atg ttg gct cat gac ggt      449
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Asn Tyr Arg Cys Thr Cys Phe Asp Gly Phe Met Leu Ala His Asp Gly	
110 115 120	
cat aat tgt ctt gat gtg gac gag tgc ctg gag aac aat ggc ggc tgc	497
His Asn Cys Leu Asp Val Asp Glu Cys Leu Glu Asn Asn Gly Gly Cys	
125 130 135	
cag cat acc tgt gtc aac gtc atg ggg agc tat gag tgc tgc tgc aag	545
Gln His Thr Cys Val Asn Val Met Gly Ser Tyr Glu Cys Cys Cys Lys	
140 145 150 155	
gag ggg ttt ttc ctg agt gac aat cag cac acc tgc att cac cgc tgc	593
Glu Gly Phe Phe Leu Ser Asp Asn Gln His Thr Cys Ile His Arg Ser	
160 165 170	
gaa gag ggc ctg agc tgc atg aat aag gat cac ggc tgt agt cac atc	641
Glu Glu Gly Leu Ser Cys Met Asn Lys Asp His Gly Cys Ser His Ile	
175 180 185	
tgc aag gag gcc cca agg ggc agc gtc gcc tgt gag tgc agg cct ggt	689
Cys Lys Glu Ala Pro Arg Gly Ser Val Ala Cys Glu Cys Arg Pro Gly	
190 195 200	
ttt gag ctg gcc aag aac cag aga gac tgc atc ttg acc tgt aac cat	737
Phe Glu Leu Ala Lys Asn Gln Arg Asp Cys Ile Leu Thr Cys Asn His	
205 210 215	
ggg aac ggt ggc tgc cag cac tcc tgt gac gat aca gcc gat ggc cca	785
Gly Asn Gly Gly Cys Gln His Ser Cys Asp Asp Thr Ala Asp Gly Pro	
220 225 230 235	
gag tgc agc tgc cat cca cag tac aag atg cac aca gat ggg agg agc	833
Glu Cys Ser Cys His Pro Gln Tyr Lys Met His Thr Asp Gly Arg Ser	
240 245 250	
tgc ctt gag cga gag gac act gtc ctg gag gtg aca gag agc aac acc	881
Cys Leu Glu Arg Glu Asp Thr Val Leu Glu Val Thr Glu Ser Asn Thr	
255 260 265	
aca tca gtg gtg gat ggg gat aaa cgg gtg aaa cgg cgg ctg ctc atg	929
Thr Ser Val Val Asp Gly Asp Lys Arg Val Lys Arg Arg Leu Leu Met	
270 275 280	
gaa acg tgt gct gtc aac aat gga ggc tgt gac cgc acc tgt aag gat	977
Glu Thr Cys Ala Val Asn Asn Gly Gly Cys Asp Arg Thr Cys Lys Asp	
285 290 295	
act tcg aca ggt gtc cac tgc agt tgt cct gtt gga ttc act ctc cag	1025
Thr Ser Thr Gly Val His Cys Ser Cys Pro Val Gly Phe Thr Leu Gln	
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ttg gat ggg aag aca tgt aaa gat att gat gag tgc cag acc cgc aat	1073
Leu Asp Gly Lys Thr Cys Lys Asp Ile Asp Glu Cys Gln Thr Arg Asn	
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gga ggt tgt gat cat ttc tgc aaa aac atc gtg ggc agt ttt gac tgc	1121
Gly Gly Cys Asp His Phe Cys Lys Asn Ile Val Gly Ser Phe Asp Cys	
335 340 345	
ggc tgc aag aaa gga ttt aaa tta tta aca gat gag aag tct tgc caa	1169
Gly Cys Lys Lys Gly Phe Lys Leu Leu Thr Asp Glu Lys Ser Cys Gln	

350	355	360	
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tat ggc ttc acc cac tgt gga gac acc aat gag tgc agc atc aac aac Tyr Gly Phe Thr His Cys Gly Asp Thr Asn Glu Cys Ser Ile Asn Asn 400 405 410			1313
gga ggc tgt cag cag gtc tgt gtg aac aca gtg ggc agc tat gaa tgc Gly Gly Cys Gln Gln Val Cys Val Asn Thr Val Gly Ser Tyr Glu Cys 415 420 425			1361
cag tgc cac cct ggg tac aag ctc cac tgg aat aaa aaa gac tgt gtg Gln Cys His Pro Gly Tyr Lys Leu His Trp Asn Lys Lys Asp Cys Val 430 435 440			1409
gaa gtg aag ggg ctc ctg ccc aca agt gtg tca ccc cgt gtg tcc ctg Glu Val Lys Gly Leu Leu Pro Thr Ser Val Ser Pro Arg Val Ser Leu 445 450 455			1457
cac tgc ggt aag agt ggt gga gga gac ggg tgc ttc ctc aga tgt cac His Cys Gly Lys Ser Gly Gly Gly Asp Gly Cys Phe Leu Arg Cys His 460 465 470 475			1505
tct ggc att cac ctc tct tca gat gtc acc acc atc agg aca agt gta Ser Gly Ile His Leu Ser Ser Asp Val Thr Thr Ile Arg Thr Ser Val 480 485 490			1553
acc ttt aag cta aat gaa ggc aag tgt agt ttg aaa aat gct gag ctg Thr Phe Lys Leu Asn Glu Gly Lys Cys Ser Leu Lys Asn Ala Glu Leu 495 500 505			1601
ttt ccc gag ggt ctg cga cca gca cta cca gag aag cac agc tca gta Phe Pro Glu Gly Leu Arg Pro Ala Leu Pro Glu Lys His Ser Ser Val 510 515 520			1649
aaa gag agc ttc cgc tac gta aac ctt aca tgc agc tct ggc aag caa Lys Glu Ser Phe Arg Tyr Val Asn Leu Thr Cys Ser Ser Gly Lys Gln 525 530 535			1697
gtc cca gga gcc cct ggc cga cca agc acc cct aag gaa atg ttt atc Val Pro Gly Ala Pro Gly Arg Pro Ser Thr Pro Lys Glu Met Phe Ile 540 545 550 555			1745
act gtt gag ttt gag ctt gaa act aac caa aag gag gtg aca gct tct Thr Val Glu Phe Glu Leu Glu Thr Asn Gln Lys Glu Val Thr Ala Ser 560 565 570			1793
tgt gac ctg agc tgc atc gta aag cga acc gag aag cgg ctc cgt aaa Cys Asp Leu Ser Cys Ile Val Lys Arg Thr Glu Lys Arg Leu Arg Lys 575 580 585			1841
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 <213> Homo sapiens

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Pro Pro Gly Arg Gly Arg Ala Ala Gly Pro Gln Glu Asp Val Asp Glu
 35 40 45

Cys Ala Gln Gly Leu Asp Asp Cys His Ala Asp Ala Leu Cys Gln Asn
 50 55 60

Thr Pro Thr Ser Tyr Lys Cys Ser Cys Lys Pro Gly Tyr Gln Gly Glu
 65 70 75 80

Gly Arg Gln Cys Glu Asp Ile Asp Glu Cys Gly Asn Glu Leu Asn Gly
 85 90 95

Gly Cys Val His Asp Cys Leu Asn Ile Pro Gly Asn Tyr Arg Cys Thr
 100 105 110

Cys Phe Asp Gly Phe Met Leu Ala His Asp Gly His Asn Cys Leu Asp
 115 120 125

Val Asp Glu Cys Leu Glu Asn Asn Gly Gly Cys Gln His Thr Cys Val
 130 135 140

Asn Val Met Gly Ser Tyr Glu Cys Cys Cys Lys Glu Gly Phe Phe Leu
 145 150 155 160

Ser Asp Asn Gln His Thr Cys Ile His Arg Ser Glu Glu Gly Leu Ser
 165 170 175

Cys Met Asn Lys Asp His Gly Cys Ser His Ile Cys Lys Glu Ala Pro
 180 185 190

Arg Gly Ser Val Ala Cys Glu Cys Arg Pro Gly Phe Glu Leu Ala Lys
 195 200 205

Asn Gln Arg Asp Cys Ile Leu Thr Cys Asn His Gly Asn Gly Gly Cys
 210 215 220

Gln His Ser Cys Asp Asp Thr Ala Asp Gly Pro Glu Cys Ser Cys His
 225 230 235 240

Pro Gln Tyr Lys Met His Thr Asp Gly Arg Ser Cys Leu Glu Arg Glu
 245 250 255

Asp Thr Val Leu Glu Val Thr Glu Ser Asn Thr Thr Ser Val Val Asp
 260 265 270

Gly Asp Lys Arg Val Lys Arg Arg Leu Leu Met Glu Thr Cys Ala Val
 275 280 285

Asn Asn Gly Gly Cys Asp Arg Thr Cys Lys Asp Thr Ser Thr Gly Val
 290 295 300

His Cys Ser Cys Pro Val Gly Phe Thr Leu Gln Leu Asp Gly Lys Thr
 305 310 315 320

Cys Lys Asp Ile Asp Glu Cys Gln Thr Arg Asn Gly Gly Cys Asp His
 325 330 335

Phe Cys Lys Asn Ile Val Gly Ser Phe Asp Cys Gly Cys Lys Lys Gly
 340 345 350

Phe Lys Leu Leu Thr Asp Glu Lys Ser Cys Gln Asp Val Asp Glu Cys
 355 360 365

Ser Leu Asp Arg Thr Cys Asp His Ser Cys Ile Asn His Pro Gly Thr
 370 375 380

Phe Ala Cys Ala Cys Asn Arg Gly Tyr Thr Leu Tyr Gly Phe Thr His
 385 390 395 400

Cys Gly Asp Thr Asn Glu Cys Ser Ile Asn Asn Gly Gly Cys Gln Gln
 405 410 415

Val Cys Val Asn Thr Val Gly Ser Tyr Glu Cys Gln Cys His Pro Gly
 420 425 430

Tyr Lys Leu His Trp Asn Lys Lys Asp Cys Val Glu Val Lys Gly Leu
 435 440 445

Leu Pro Thr Ser Val Ser Pro Arg Val Ser Leu His Cys Gly Lys Ser

450	455	460
Gly Gly Gly Asp Gly Cys Phe Leu Arg Cys His Ser Gly Ile His Leu		
465	470	475 480
Ser Ser Asp Val Thr Thr Ile Arg Thr Ser Val Thr Phe Lys Leu Asn		
	485	490 495
Glu Gly Lys Cys Ser Leu Lys Asn Ala Glu Leu Phe Pro Glu Gly Leu		
	500	505 510
Arg Pro Ala Leu Pro Glu Lys His Ser Ser Val Lys Glu Ser Phe Arg		
	515	520 525
Tyr Val Asn Leu Thr Cys Ser Ser Gly Lys Gln Val Pro Gly Ala Pro		
	530	535 540
Gly Arg Pro Ser Thr Pro Lys Glu Met Phe Ile Thr Val Glu Phe Glu		
545	550	555 560
Leu Glu Thr Asn Gln Lys Glu Val Thr Ala Ser Cys Asp Leu Ser Cys		
	565	570 575
Ile Val Lys Arg Thr Glu Lys Arg Leu Arg Lys Ala Ile Arg Thr Leu		
	580	585 590
Arg Lys Ala Val His Arg Glu Gln Phe His Leu Gln Leu Ser Gly Met		
	595	600 605
Asn Leu Asp Val Ala Lys Lys Pro Pro Arg Thr Ser Glu Arg Gln Ala		
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Glu Ser Cys Gly Val Gly Gln Gly His Ala Glu Asn Gln Cys Val Ser		
625	630	635 640
Cys Arg Ala Gly Thr Tyr Tyr Asp Gly Ala Arg Glu Arg Cys Ile Leu		
	645	650 655
Cys Pro Asn Gly Thr Phe Gln Asn Glu Glu Gly Gln Met Thr Cys Glu		
	660	665 670
Pro Cys Pro Arg Pro Gly Asn Ser Gly Ala Leu Lys Thr Pro Glu Ala		
	675	680 685
Trp Asn Met Ser Glu Cys Gly Gly Leu Cys Gln Pro Gly Glu Tyr Ser		
690	695	700

Ala Asp Gly Phe Ala Pro Cys Gln Leu Cys Ala Leu Gly Thr Phe Gln
705 710 715 720

Pro Glu Ala Gly Arg Thr Ser Cys Phe Pro Cys Gly Gly Gly Leu Ala
725 730 735

Thr Lys His Gln Gly Ala Thr Ser Phe Gln Asp Cys Glu Thr Arg Val
740 745 750

Gln Cys Ser Pro Gly His Phe Tyr Asn Thr Thr Thr His Arg Cys Ile
755 760 765

Arg Cys Pro Val Gly Thr Tyr Gln Pro Glu Phe Gly Lys Asn Asn Cys
770 775 780

Val Ser Cys Pro Gly Asn Thr Thr Thr Asp Phe Asp Gly Ser Thr Asn
785 790 795 800

Ile Thr Gln Cys Lys Asn Arg Arg Cys Gly Gly Glu Leu Gly Asp Phe
805 810 815

Thr Gly Tyr Ile Glu Ser Pro Asn Tyr Pro Gly Asn Tyr Pro Ala Asn
820 825 830

Thr Glu Cys Thr Trp Thr Ile Asn Pro Pro Pro Lys Arg Arg Ile Leu
835 840 845

Ile Val Val Pro Glu Ile Phe Leu Pro Ile Glu Asp Asp Cys Gly Asp
850 855 860

Tyr Leu Val Met Arg Lys Thr Ser Ser Ser Asn Ser Val Thr Thr Tyr
865 870 875 880

Glu Thr Cys Gln Thr Tyr Glu Arg Pro Ile Ala Phe Thr Ser Arg Ser
885 890 895

Lys Lys Leu Trp Ile Gln Phe Lys Ser Asn Glu Gly Asn Ser Ala Arg
900 905 910

Gly Phe Gln Val Pro Tyr Val Thr Tyr Asp Glu Asp Tyr Gln Glu Leu
915 920 925

Ile Glu Asp Ile Val Arg Asp Gly Arg Leu Tyr Ala Ser Glu Asn His
930 935 940

Gln Glu Ile Leu Lys Asp Lys Lys Leu Ile Lys Ala Leu Phe Asp Val
 945 950 955 960

Leu Ala His Pro Gln Asn Tyr Phe Lys Tyr Thr Ala Gln Glu Ser Arg
 965 970 975

Glu Met Phe Pro Arg Ser Phe Ile Arg Leu Leu Arg Ser Lys Val Ser
 980 985 990

Arg Phe Leu Arg Pro Tyr Lys
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Asp Arg Gly Leu Thr Asn Gly Pro Ser Glu Asp Val Asp Glu Cys Ala
 35 40 45

Gln Gly Leu Asp Asp Cys His Ala Asp Ala Leu Cys Gln Asn Thr Pro
 50 55 60

Thr Ser Tyr Lys Cys Ser Cys Lys Pro Gly Tyr Gln Gly Glu Gly Arg
 65 70 75 80

Gln Cys Glu Asp Met Asp Glu Cys Asp Asn Thr Leu Asn Gly Gly Cys
 85 90 95

Val His Asp Cys Leu Asn Ile Pro Gly Asn Tyr Arg Cys Thr Cys Phe
 100 105 110

Asp Gly Phe Met Leu Ala His Asp Gly His Asn Cys Leu Asp Met Asp
 115 120 125

Glu Cys Leu Glu Asn Asn Gly Gly Cys Gln His Ile Cys Thr Asn Val
 130 135 140

Ile Gly Ser Tyr Glu Cys Arg Cys Lys Glu Gly Phe Phe Leu Ser Asp
 145 150 155 160

Asn Gln His Thr Cys Ile His Arg Ser Glu Glu Gly Leu Ser Cys Met
 165 170 175

Asn Lys Asp His Gly Cys Gly His Ile Cys Lys Glu Ala Pro Arg Gly
 180 185 190

Ser Val Ala Cys Glu Cys Arg Pro Gly Phe Glu Leu Ala Lys Asn Gln

Asn	Leu	Thr	Cys	Ser	Pro	Gly	Lys	Gln	Val	Pro	Gly	Ala	Leu	Gly	Arg	530	535	540	
Leu	Asn	Ala	Pro	Lys	Glu	Met	Phe	Ile	Thr	Val	Glu	Phe	Glu	Arg	Glu	545	550	555	560
Thr	Tyr	Glu	Lys	Glu	Val	Thr	Ala	Ser	Cys	Asn	Leu	Ser	Cys	Val	Val	565	570	575	
Lys	Arg	Thr	Glu	Lys	Arg	Leu	Arg	Lys	Ala	Leu	Arg	Thr	Leu	Lys	Arg	580	585	590	
Ala	Ala	His	Arg	Glu	Gln	Phe	His	Leu	Gln	Leu	Ser	Gly	Met	Asp	Leu	595	600	605	
Asp	Met	Ala	Lys	Thr	Pro	Ser	Arg	Val	Ser	Gly	Gln	His	Glu	Glu	Thr	610	615	620	
Cys	Gly	Val	Gly	Gln	Gly	His	Glu	Glu	Ser	Gln	Cys	Val	Ser	Cys	Arg	625	630	635	640
Ala	Gly	Thr	Tyr	Tyr	Asp	Gly	Ser	Gln	Glu	Arg	Cys	Ile	Leu	Cys	Pro	645	650	655	
Asn	Gly	Thr	Phe	Gln	Asn	Glu	Glu	Gly	Gln	Val	Thr	Cys	Glu	Pro	Cys	660	665	670	
Pro	Arg	Pro	Glu	Asn	Leu	Gly	Ser	Leu	Lys	Ile	Ser	Glu	Ala	Trp	Asn	675	680	685	
Val	Ser	Asp	Cys	Gly	Gly	Leu	Cys	Gln	Pro	Gly	Glu	Tyr	Ser	Ala	Asn	690	695	700	
Gly	Phe	Ala	Pro	Cys	Gln	Leu	Cys	Ala	Leu	Gly	Thr	Phe	Gln	Pro	Asp	705	710	715	720
Val	Gly	Arg	Thr	Ser	Cys	Leu	Ser	Cys	Gly	Gly	Gly	Leu	Pro	Thr	Lys	725	730	735	
His	Leu	Gly	Ala	Thr	Ser	Phe	Gln	Asp	Cys	Glu	Thr	Arg	Val	Gln	Cys	740	745	750	
Ser	Pro	Gly	His	Phe	Tyr	Asn	Thr	Thr	Thr	His	Arg	Cys	Ile	Arg	Cys	755	760	765	
Pro	Leu	Gly	Thr	Tyr	Gln	Pro	Glu	Phe	Gly	Lys	Asn	Asn	Cys	Val	Ser	770	775	780	
Cys	Pro	Gly	Asn	Thr	Thr	Thr	Asp	Phe	Asp	Gly	Ser	Thr	Asn	Ile	Thr	785	790	795	800
Gln	Cys	Lys	Asn	Arg	Lys	Cys	Gly	Gly	Glu	Leu	Gly	Asp	Phe	Thr	Gly	805	810	815	
Tyr	Ile	Glu	Ser	Pro	Asn	Tyr	Pro	Gly	Asn	Tyr	Pro	Ala	Asn	Ser	Glu	820	825	830	
Cys	Thr	Trp	Thr	Ile	Asn	Pro	Pro	Pro	Lys	Arg	Arg	Ile	Leu	Ile	Val	835	840	845	

Val Pro Glu Ile Phe Leu Pro Ile Glu Asp Asp Cys Gly Asp Tyr Leu
850 855 860

Val Met Arg Lys Thr Ser Ser Ser Asn Ser Val Thr Thr Tyr Glu Thr
865 870 875 880

Cys Gln Thr Tyr Glu Arg Pro Ile Ala Phe Thr Ser Arg Ser Lys Lys
885 890 895

Leu Trp Ile Gln Phe Lys Ser Asn Glu Gly Asn Ser Ala Arg Gly Phe
900 905 910

Gln Val Pro Tyr Val Thr Tyr Asp Glu Asp Tyr Gln Glu Leu Ile Glu
915 920 925

Asp Ile Val Arg Asp Gly Arg Leu Tyr Ala Ser Glu Asn His Gln Glu
930 935 940

Ile Leu Lys Asp Lys Lys Leu Ile Lys Ala Leu Phe Asp Val Leu Ala
945 950 955 960

His Pro Gln Asn Tyr Phe Lys Tyr Thr Ala Gln Glu Ser Arg Glu Met
965 970 975

Phe Pro Arg Ser Phe Ile Arg Leu Leu Arg Ser Lys Val Ser Arg Phe
980 985 990

Leu Arg Pro Tyr Lys
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<213> Unknown

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<223> Cytokine receptor extracellular motif found in many species.

<220>

<221> UNSURE

<222> (3)..(3)

<223> "Xaa" at position 3 can be any amino acid.

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Trp Ser Xaa Trp Ser
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